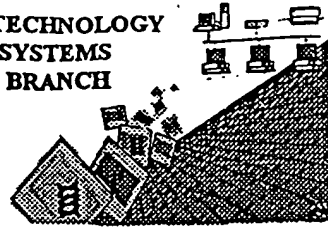


5040

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/517,324

Source:

PGT

Date Processed by STIC:

12-28-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/5171324

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<22> section that some may be missing
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>.<22> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<22> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<22> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
                    (i)     SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)  
                    (xi)  SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>.<22> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <22> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<22> section is required when <213> response is Unknown or Artificial Sequence.
- 11      Use of <220>     Use of <220> to <22> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <22> section.  
                    (Sec "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

## RAW SEQUENCE LISTING

DATE: 12/28/2004

PATENT APPLICATION: US/10/517,324

TIME: 11:50:05

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

3 <110> APPLICANT: SinoGenoMax Company Ltd  
 5 <120> TITLE OF INVENTION: Randomised DNA libraries and double-stranded RNA libraries,  
 use and

6 method of production thereof

8 &lt;130&gt; FILE REFERENCE: P06031PC00

C--&gt; 10 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/517,324

C--&gt; 11 &lt;141&gt; CURRENT FILING DATE: 2004-12-20

13 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/390,108

14 &lt;151&gt; PRIOR FILING DATE: 2002-06-21

16 &lt;160&gt; NUMBER OF SEQ ID NOS: 45

18 &lt;170&gt; SOFTWARE: PatentIn version 3.1

20 &lt;210&gt; SEQ ID NO: 1

21 &lt;211&gt; LENGTH: 29

22 &lt;212&gt; TYPE: DNA

23 &lt;213&gt; ORGANISM: Artificial Sequence

25 &lt;220&gt; FEATURE:

26 &lt;223&gt; OTHER INFORMATION: 5?rimer

28 &lt;400&gt; SEQUENCE: 1

29 ggaattcgaa cgctgacgtc atcaaccg

32 &lt;210&gt; SEQ ID NO: 2

33 &lt;211&gt; LENGTH: 35

34 &lt;212&gt; TYPE: DNA

35 &lt;213&gt; ORGANISM: Artificial Sequence

37 &lt;220&gt; FEATURE:

38 &lt;223&gt; OTHER INFORMATION: 3?rimer

40 &lt;400&gt; SEQUENCE: 2

41 gaagatctgt ctcatacaga acttataaga ttccc

44 &lt;210&gt; SEQ ID NO: 3

45 &lt;211&gt; LENGTH: 500

46 &lt;212&gt; TYPE: DNA

47 &lt;213&gt; ORGANISM: Artificial Sequence

49 &lt;220&gt; FEATURE:

50 &lt;223&gt; OTHER INFORMATION: Modified sequence

52 &lt;220&gt; FEATURE:

53 &lt;221&gt; NAME/KEY: misc\_feature

54 &lt;222&gt; LOCATION: (7)..(7)

55 <223> OTHER INFORMATION: Represents nucleotides not clearly identified in the  
 sequencing r

56 result.

59 &lt;220&gt; FEATURE:

60 &lt;221&gt; NAME/KEY: misc\_feature

61 &lt;222&gt; LOCATION: (9)..(9)

62 <223> OTHER INFORMATION: Represents nucleotides not clearly identified in the  
 sequencing r

Does Not Comply  
 Corrected Diskette Needed

(pg. 1-4/6)

Pls explain source of  
 genetic material.

Invalid  
 response

29

Pls explain source of genetic  
 material.

Invalid  
 response

35

Pls explain source of genetic  
 material.

Invalid response

See  
 item  
 #11

Invalid response

On error  
 Summary  
 sheet.

"N" can only represent a  
 single nucleotide.

63

result

66 <400> SEQUENCE: 3

part of  
- see error explanation on ps. 1.

pls explain "N" locations.

## RAW SEQUENCE LISTING

DATE: 12/28/2004

PATENT APPLICATION: US/10/517,324

TIME: 11:50:05

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

W--> 67 tccaggaac gcgggccag tgtcactagg cgggaacacc cagcgcgct ggcgcctggc 60  
 69 aggaagatgg ctgtgagga caggggagtg gcgcctgca atattgcat gtcgctatgt 120  
 71 gttctgggaa atcaccataa acgtgaaatg tctttggatt tgggaatctt ataagttctg 180  
 73 tatgagacag atcttcaata ttggccatta gccatattat tcattgggta tatagcataa 240  
 75 atcaatattg gctattggcc attgcatacg ttgtatctat atcataatat gtacatttat 300  
 77 attggctcat gtccaatatg accgccatgt tggcattgat tattgactag ttattaatag 360  
 79 taatcaatta cggggtcatt agttcatagc ccattatggg agttccgctg tacataactt 420  
 81 acggtaaatg gcccgcctgg ctgaccgcc aacgaccccc gccattgac gtcaataatg 480  
 83 acgtatgttc ccatagtaac 500  
 86 <210> SEQ ID NO: 4  
 87 <211> LENGTH: 38  
 88 <212> TYPE: DNA  
 89 <213> ORGANISM: Artificial Sequence  
 91 <220> FEATURE:  
 92 <223> OTHER INFORMATION: 5?rimer *same error*  
 94 <400> SEQUENCE: 4  
 95 acgcgtcgac gaattcgaac gctgacgtca tcaacccg 38  
 98 <210> SEQ ID NO: 5  
 99 <211> LENGTH: 36  
 100 <212> TYPE: DNA  
 101 <213> ORGANISM: Artificial Sequence  
 103 <220> FEATURE:  
 104 <223> OTHER INFORMATION: 3?rimer *same error*  
 106 <400> SEQUENCE: 5  
 107 cccaagcttg tctcatacag aacttataag attccc 36  
 110 <210> SEQ ID NO: 6  
 111 <211> LENGTH: 50  
 112 <212> TYPE: DNA  
 113 <213> ORGANISM: Artificial Sequence  
 115 <220> FEATURE:  
 116 <223> OTHER INFORMATION: oligo DNA  
 118 <400> SEQUENCE: 6  
 119 ggggaagatc taaaaaata aatgaatcaa gaacattttt aagcttgggg 50  
 122 <210> SEQ ID NO: 7  
 123 <211> LENGTH: 50  
 124 <212> TYPE: DNA  
 125 <213> ORGANISM: Artificial Sequence  
 127 <220> FEATURE:  
 128 <223> OTHER INFORMATION: oligo DNA  
 130 <400> SEQUENCE: 7  
 131 ccccaagctt aaaaatgttc ttgattcatt tattttttta gatcttcccc 50  
 134 <210> SEQ ID NO: 8  
 135 <211> LENGTH: 50  
 136 <212> TYPE: DNA  
 137 <213> ORGANISM: Artificial Sequence  
 139 <220> FEATURE:  
 140 <223> OTHER INFORMATION: 19 nucleotides randomized region  
 142 <220> FEATURE:  
 143 <221> NAME/KEY: misc\_feature

What is the source of genetic material?

Invalid response

See item # 11 on error summary sheet. 12/28/04

TIME: 11:50:05

Output Set: N:\CRF4\12282004\J517324.raw

217 <220> FEATURE:

same errors

Only represent  
51 a single nucleotide.

## RAW SEQUENCE LISTING

DATE: 12/28/2004

PATENT APPLICATION: US/10/517,324

TIME: 11:50:05

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

```

218 <223> OTHER INFORMATION: 19 base pair clone
220 <400> SEQUENCE: 13
221 aatcgtctta tttgcatgc 19
224 <210> SEQ ID NO: 14
225 <211> LENGTH: 19
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: 19 base pair clone
232 <400> SEQUENCE: 14
233 aattgacatg tgagcttgg 19
236 <210> SEQ ID NO: 15
237 <211> LENGTH: 19
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: 19 base pair clone
244 <400> SEQUENCE: 15
245 agtagcttgt tgaggttgg 19
248 <210> SEQ ID NO: 16
249 <211> LENGTH: 19
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: 19 base pair clone
256 <400> SEQUENCE: 16
257 cagcatcact gtatgtgtc 19
260 <210> SEQ ID NO: 17
261 <211> LENGTH: 19
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: 19 base pair clone
268 <400> SEQUENCE: 17
269 ctatcttcgt ggaggttgg 19
272 <210> SEQ ID NO: 18
273 <211> LENGTH: 19
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: 19 base pair clone
280 <400> SEQUENCE: 18
281 ctatgaaggt ggtgatgcg 19
284 <210> SEQ ID NO: 19
285 <211> LENGTH: 19
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: 19 base pair clone

```

DATE: 12/28/2004

TIME: 11:50:05

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

```

292 <400> SEQUENCE: 19
293 cttaattggt gggtgtagg
296 <210> SEQ ID NO: 20
297 <211> LENGTH: 19
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: 19 base pair clone
304 <400> SEQUENCE: 20
305 tggctgtatg tgagtggct
308 <210> SEQ ID NO: 21
309 <211> LENGTH: 19
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial Sequence
313 <220> FEATURE:
314 <223> OTHER INFORMATION: 19 base pair clone
316 <400> SEQUENCE: 21
317 ttaatctctg gtgtcctaa
320 <210> SEQ ID NO: 22
321 <211> LENGTH: 19
322 <212> TYPE: DNA
323 <213> ORGANISM: Artificial Sequence
325 <220> FEATURE:
326 <223> OTHER INFORMATION: 19 base pair clone
328 <400> SEQUENCE: 22
329 ttgtagggac ttggatgat
332 <210> SEQ ID NO: 23
333 <211> LENGTH: 15
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Primer
340 <400> SEQUENCE: 23
341 aaaaattcga acccc
344 <210> SEQ ID NO: 24
345 <211> LENGTH: 50
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: (complementary to SEQ ID NO 8)
352 <220> FEATURE:
353 <221> NAME/KEY: misc_feature
354 <222> LOCATION: (17)..(35)
355 <223> OTHER INFORMATION: (Randomized region.)
358 <400> SEQUENCE: 24
359 ccccttctag attttt nnnnnnnnnn nnnnnnaaaaa ttcgaacccc
362 <210> SEQ ID NO: 25
363 <211> LENGTH: 35
364 <212> TYPE: DNA

```

same errors

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/517,324

DATE: 12/28/2004  
TIME: 11:50:06

Input Set : A:\040679.txt  
Output Set : N:\CRF4\12282004\J517324.raw

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 7,9 ✓  
Seq#:8; N Pos. 17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35  
Seq#:9; N Pos. 17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36  
Seq#:10; N Pos. 17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36  
Seq#:10; N Pos. 37  
Seq#:24; N Pos. 17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35  
Seq#:25; N Pos. 11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29  
Seq#:26; N Pos. 7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25  
Seq#:34; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19  
Seq#:38; N Pos. 8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,36  
Seq#:38; N Pos. 37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54  
Seq#:39; N Pos. 4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,32,33,34  
Seq#:39; N Pos. 35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50  
Seq#:42; N Pos. 8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26  
Seq#:43; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19  
Seq#:44; N Pos. 4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22  
Seq#:45; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19

## VERIFICATION SUMMARY

DATE: 12/28/2004

PATENT APPLICATION: US/10/517,324

TIME: 11:50:06

Input Set : A:\040679.txt

Output Set: N:\CRF4\12282004\J517324.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0  
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0  
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0  
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0  
L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0  
L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0  
L:627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0  
L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0  
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0  
L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0